```
                                                                                                                                          119
   1   AGCAGACAGAGGACTCTCATTAAGGAAGG TGTCCTGTGCCCTGACCCTACAAGATGCCA AGAGAAGATGCTCACTTCATCTATGGTTAC CCCAAGAAGGGGCACGGCCACTCTTACACC    22
                                                         MetPro ArgGluAspAlaHisPheIleTyrGlyTyr ProLysLysGlyHisGlyHisSerTyrThr

                                                                                                                                          239
 120   ACGGCTGAAGAGGCCGCTGGGATCGGCATC CTGACAGTGATCCTGGGAGTCTTACTGCTC ATCGGCTGTTGGTATTGTAGAAGACGAAAT GGATACAGAGCCTTGATGGATAAAAGTCTT    62
  23   ThrAlaGluGluAlaAlaGlyIleGlyIle LeuThrValIleLeuGlyValLeuLeuLeu IleGlyCysTrpTyrCysArgArgArgAsn GlyTyrArgAlaLeuMetAspLysSerLeu

                                                                                                                                          359
 240   CATGTTGGCACTCAATGTGCCTTAACAAGA AGATGCCCACAAGAAGGGTTTGATCATCGG GACAGCAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCCAATGCTCCACCT   102
  63   HisValGlyThrGlnCysAlaLeuThrArg ArgCysProGlnGluGlyPheAspHisArg AspSerLysValSerLeuGlnGluLysAsn CysGluProValValProAsnAlaProPro

                                                                                                                                          479
 360   GCTTATGAGAAACTCTCTGCAGAACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG AGACACCTGAGACATGCTGAAATTATTTCT CTCACACTTTTGCTTGAATTTAATACAGAC   118
 103   AlaTyrGluLysLeuSerAlaGluGlnSer ProProProTyrSerPro

 480   ATCTAATGTTCTCCTTTGGAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC AGTGTTAAAATTTTAGTAGGTCCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA   599
 600   TATTAAATTGGGAAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA GGTAATGTTAGTAAATCCATGGTGTTATTT TCTGAGAGACAGAATTCAAGTGGGTATTCT   719
 720   GGGGCCATCCAATTTCTCTTTACTTGAAAT TTGGCTAATAACAAACTAGTCAGGTTTTCG AACCTTGACCGACATGAACTGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG   839
 840   GATACTTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT CAGCAATGTCTCTTTGTGCTCTAAAATTCT ATTATACTACAATAATATATTGTAAAGATC   959
 960   CTATAGCTCTTTTTTTTTGAGATGGAGTTT CGCTTTTGTTGCCCAGGCTGGAGTGCAATG GCGCGATCTTGGCTCACCATAACCTCCGCC TCCCAGGTTCAAGCAATTCTCCTGCCTTAG  1079
1080   CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTTT AGTAGAGACGGGGTTTCTCCATGTTGGTCA GGCTGGTCTCAAACTCCTGACCTCAGGTGA  1199
1200   TCTGCCCGCCTCAGCCTCCCAAAGTGCTGG AATTACAGGCGTGAGCCACCACGCCTGGCT GGATCCTATATCTTAGGTAAGACATATAAC GCAGTCTAATTACATTTCACTTCAAGGCTC  1319
1320   AATGCTATTCTAACTAATGACAAGTATTTT CTACTAAACCAGAAATTGGTAGAAGGATTT AAATAAGTAAAAGCTACTATGTACTGCCTT AGTGCTGATGCCTGTGTACTGCCTTAAATG  1439
1440   TACCTATGGCAATTTAGCTCTCTTGGGTTC CCAAATCCCTCTCACAAGAATGTGCAGAAG AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  1559
```

FIGURE 1

EJ083359791US

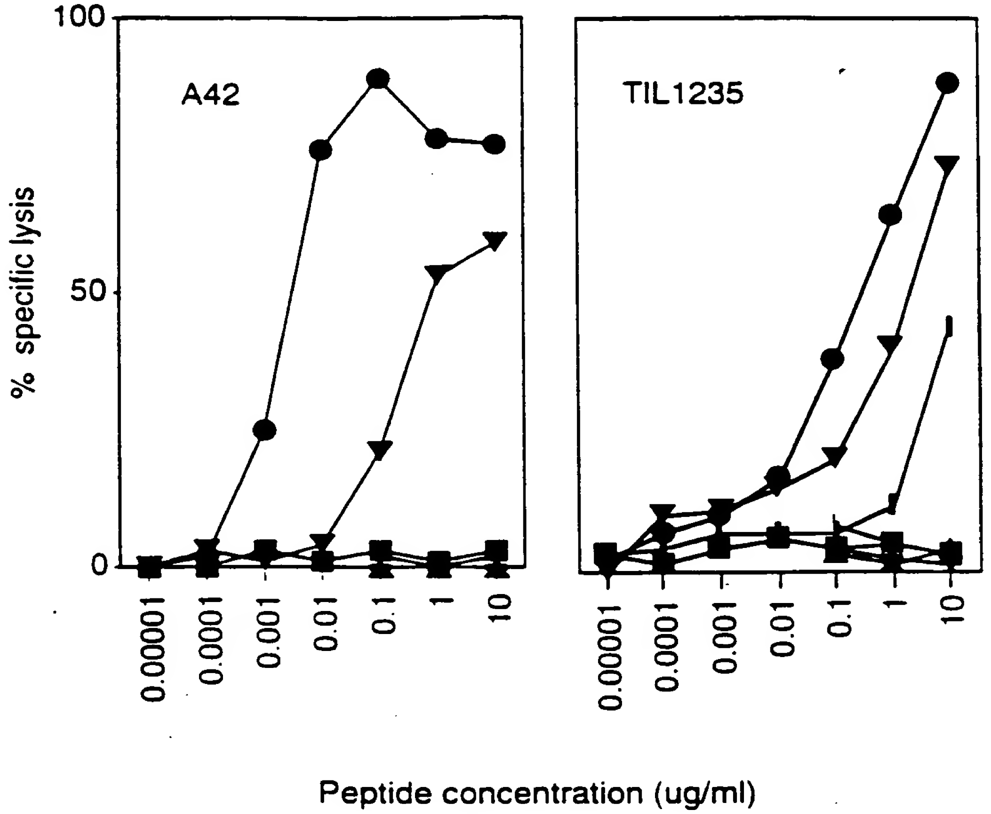

A42
TIL1235
100
50
0
% specific lysis
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIGURE 2

09267439.031299

FIGURE 3A

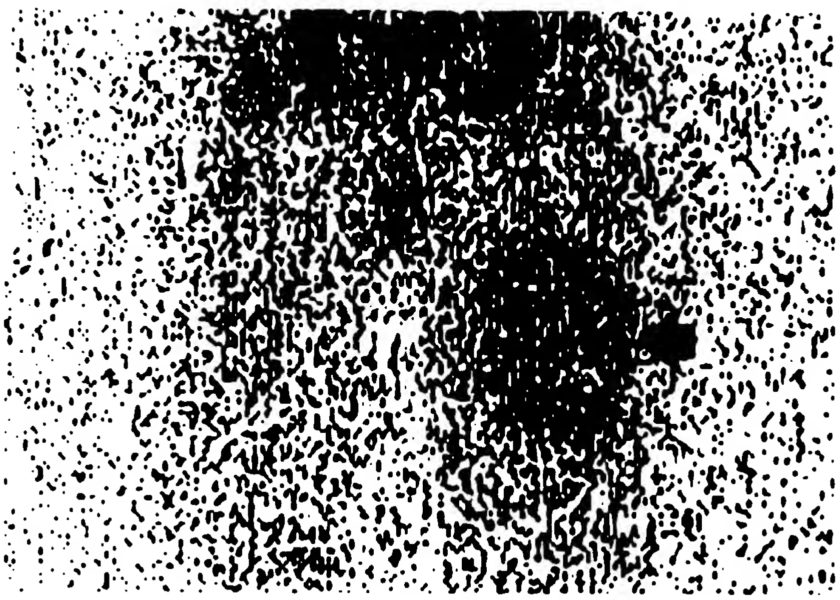
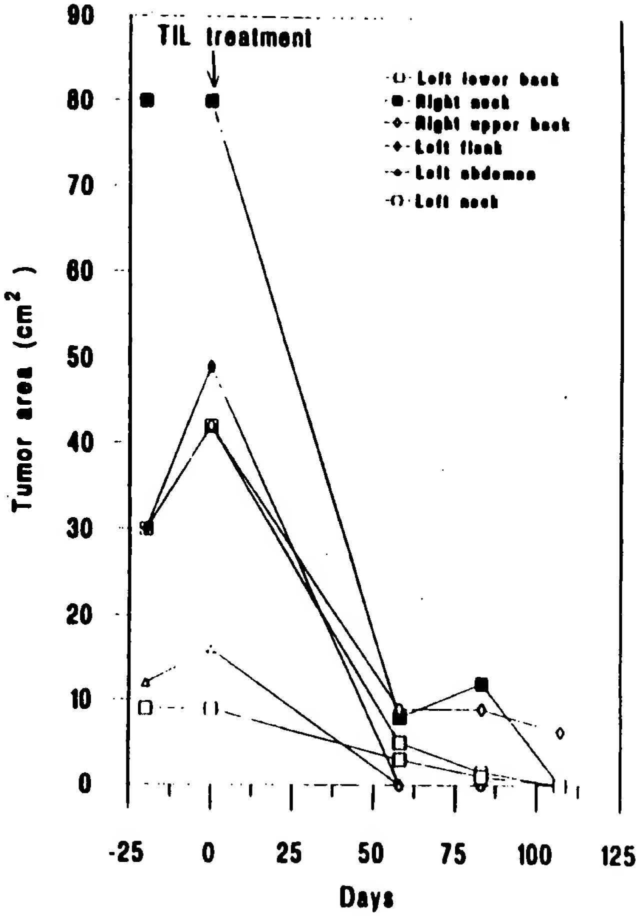


FIGURE 3B



EJ083359791US

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT 40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG 80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA 120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC 160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA 200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC 240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA 280
TGCCTCCTTC TCTATTGCCT TGAACTTCCC TGGAAGCCAA 320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA 360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT 400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT 440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA 480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA 520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA 560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG 600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC 640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT 680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG 720
GGAACAAGCA CTTCCTGAGA AATCAGCCTC TGACCTTTGC 760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT 800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA 840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT 880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT 920
GCCATTCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG 960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA 1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT 1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA 1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC 1120

FIGURE 4

```
TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG     116
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA     120
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC     124
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA     1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG     1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC     1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG     1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA     1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG     1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA     1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG     1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC     1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG     1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC     1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG     1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC     1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG     1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG     1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG     1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC     1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC     1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC     2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG     2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC     2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT     2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA     2160
AAAAAAAAAA AA                                   2172
```

FIGURE 4 (continued)

FIGURE 5A

```
  1   MDLVLKRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRQLR TKAWNRQLYP
 51   EWTEAQRLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLPDG
101   QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151   YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201   AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
251   LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301   CGSSPVPGTT DGHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
351   VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401   TPAEVSIVVL SGTTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451   TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501   AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQRL CQPVLPSPAC
551   QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601   GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651   ENSPLLSGQQ V
```

FIGURE 5B

```
Pmel17     M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20       M-----V-----Q-----L-----  ......-------------
gp100      M-----V-----Q-----L-----.......------------
cDNA25FL   M-----F-----Q-----L-----.......------------
cDNA25TR               Q-----L-----..........-----PPQWAAGLSTLI
           1    162   236   274   588           649
```

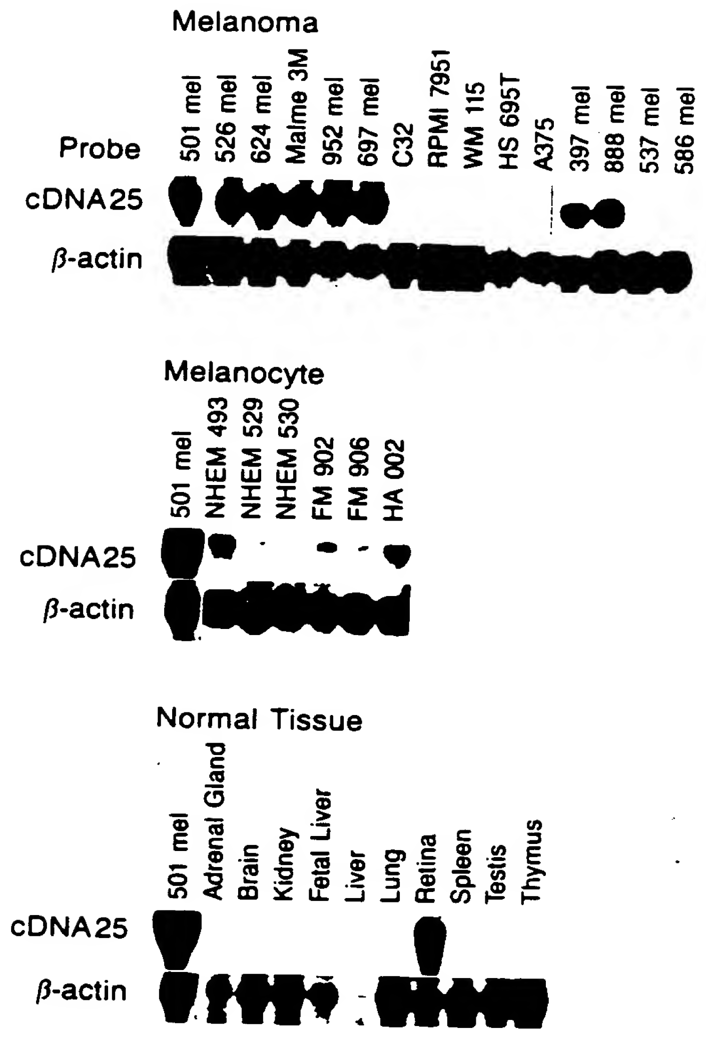


FIGURE 6

09274399.032599